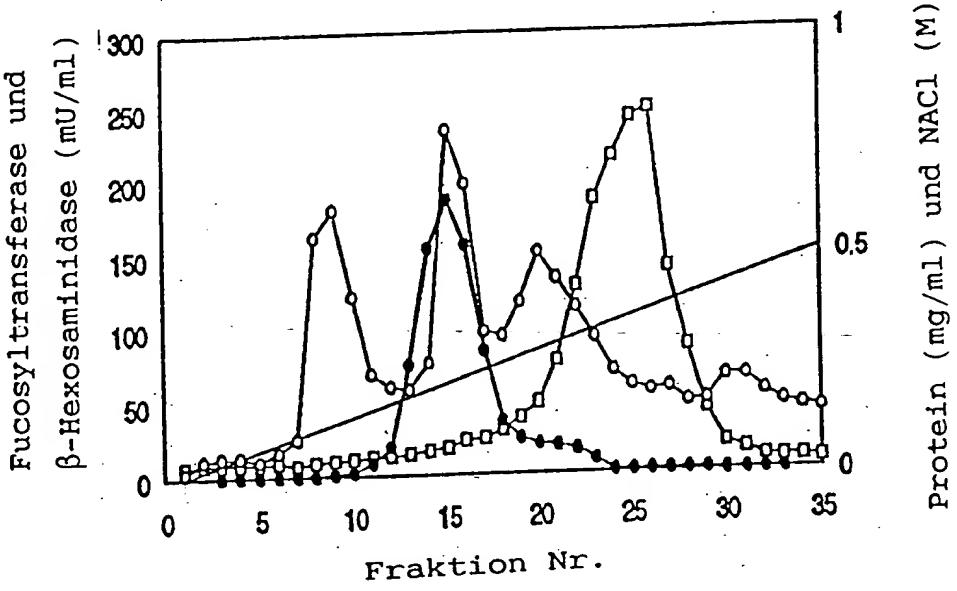


FIG.1 a

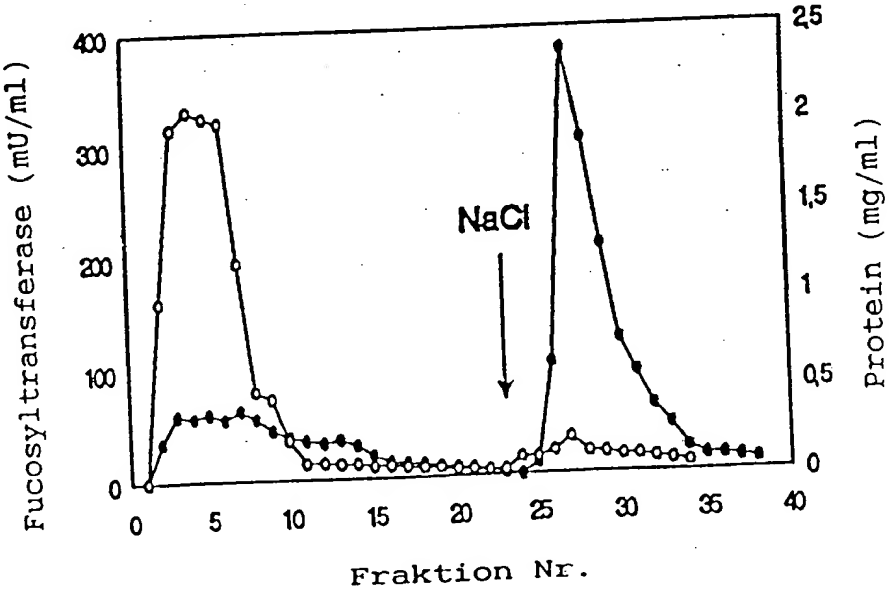


FIG.1 b

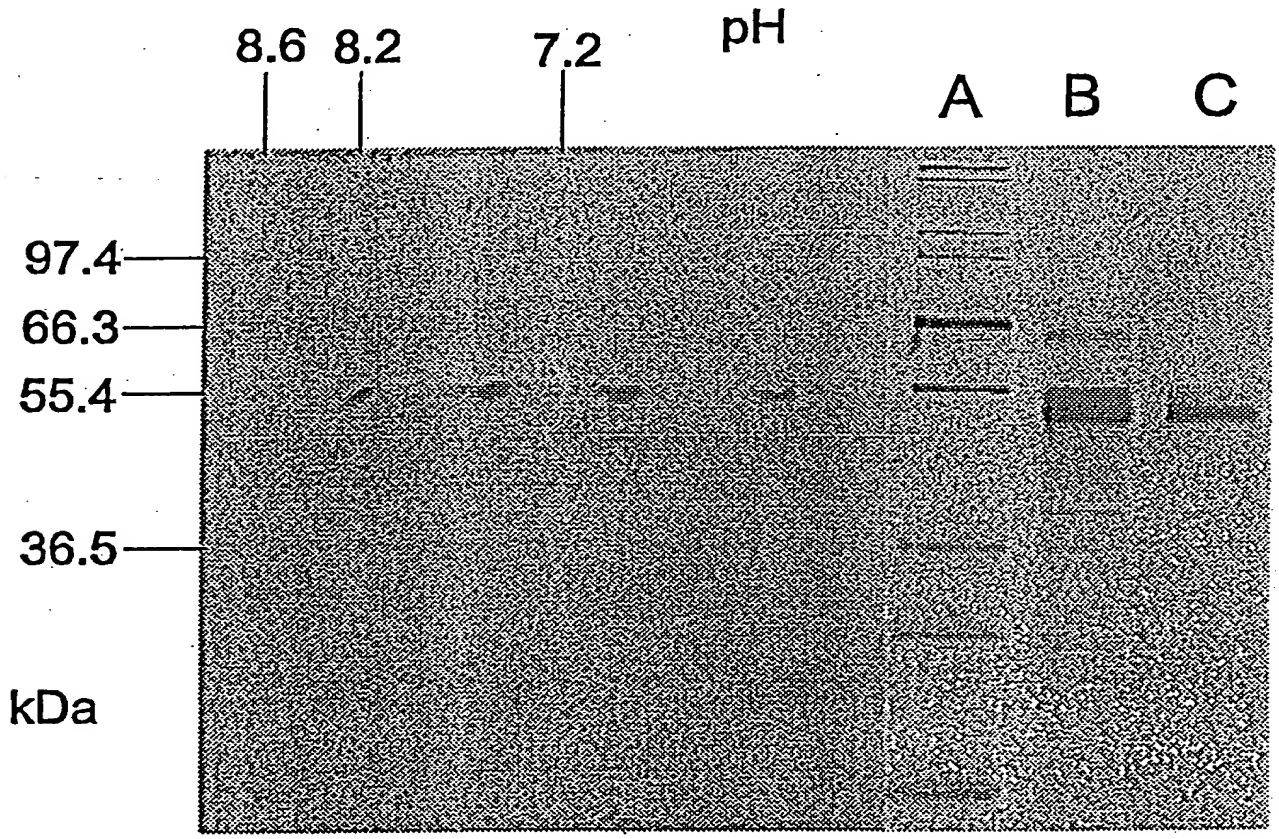
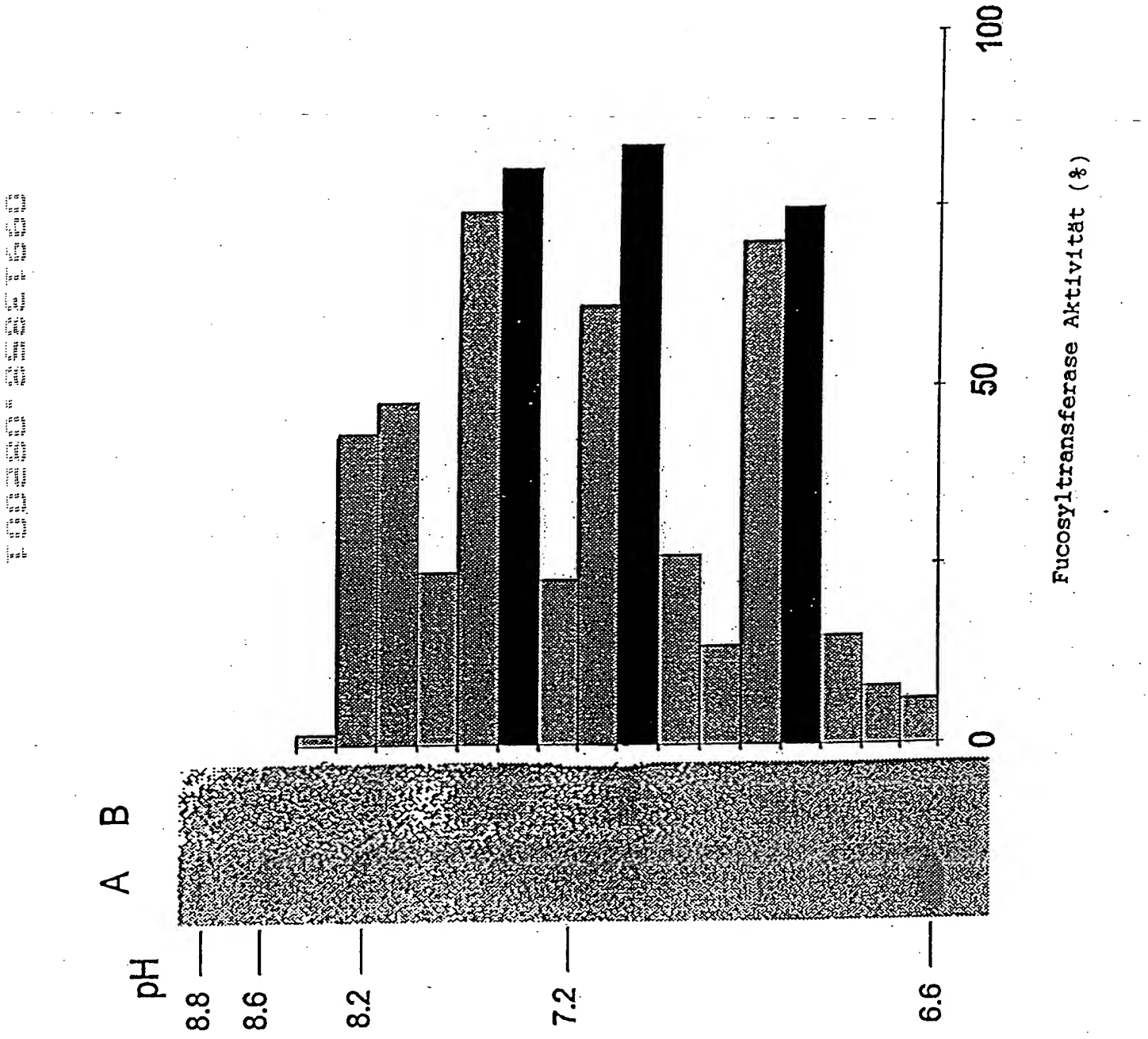


FIG.2

FIG.3



1 KPDAxFGLPQPSTAS

2 PETVYHIYVR

3 MESAEYYAENNIA

4 GRFEMESIYL

S1 5′- GCIGAATACTACGCIGAAAACAACATCGC -3′
A
G T T G T T T

A2 5′- CATAGATATGATAIACIGTCTC -3′
A
G T G G T

A3 5′- TAGATICACTCCATCTCAAA - 3′
A
T GTT T G

FIG.4

```
ACTAACTCAA ACGCTGCATT TTCTTTTTTC TTTCAGGGAA CCATCCACCC ATAACAACAA      60
AAAAAACAAC AGCAAGCTGT GTTTTTTTTA TCGTTCTTTT TCTTTAAACA AGCACCCCCA     120
TCATGGAATC GTGCTCATAA CGCCAAAATT TTCCATTTCC CTTTGATTTT TAGTTTATTT     180
TGCGGAATTG GCAGTTGGGG GCGCAATTGA ATGATGGGTC TGTTGACGAA TCTTCGAGGC     240
TCGAGAACAG ATGGTGCCCA ACAAGACAGC TTACCCGTTT TGGCTCCGGG AGGCAACCCA     300
AAGAGGAAAT GGAGCAATCT AATGCCTCTT GTTGTTGCCC TTGTGGTCAT CGCGGAGATC     360
GCGTTTCTGG GTAGGTTGGA TATGGCCAAA AACGCCGCCA TGGTTGACTC CCTCGCTGAC     420
TTCTTCTACC GCTCTCGAGC GGTCGTTGAA GGTGACGATT TGGGGTTGGG TTTGGTGGCT     480
TCTGATCGGA ATTCTGAATC GTATAGTTGT GAGGAATGGT TGGAGAGGGA GGATGCTGTC     540
ACGTATTCGA GGGGCTTTTC CAAAGAGCCT ATTTTTGTTT CTGGAGCTGA TCAGGAGTGG     600
AAGTCGTGTT CGGTTGGATG TAAATTTGGG TTTAGTGGGG ATAGAAAGCC AGATGCCGCA     660
TTTGGGTTAC CTCAACCAAG TGGAACAGCT AGCATTCTGC GATCAATGGA ATCAGCAGAA     720
TACTATGCTG AGAACAATAT TGCCATGGCA AGACGGAGGG GATATAACAT CGTAATGACA     780
ACCAGTCTAT CTTCGGATGT TCCTGTTGGA TATTTTTCAT GGGCTGAGTA TGATATGATG     840
GCACCAGTGC AGCCGAAAAC TGAAGCTGCT CTTGCAGCTG CTTTCATTTC CAATTGTGGT     900
GCTCGAAATT TCCGGTTGCA AGCTCTTGAG GCCCTTGAAA AATCAAACAT CAAAATTGAT     960
TCTTATGGTG GTTGTCACAG GAACCGTGAT GGAAGAGTGA ACAAAGTGGA AGCCCTGAAG    1020
CACTACAAAT TTAGCTTAGC GTTTGAAAAT TCGAATGAGG AAGATTATGT AACTGAAAAA    1080
TTCTTCCAAT CCCTTGTTGC TGGAACTGTC CCTGTGGTTG TTGGTGCTCC AAATATTCAG    1140
```

FIG.5 a

GACTTTGCTC CTTCTCCTGG TTCAATTTTA CATATTAAAG AGATAGAGGA TGTTGAGTCT 1200

GTTGCAAAGA CCATGAGATA TCTAGCAGAA AATCCCGAAG CATATAATCA ATCATTGAGG 1260

TGGAAGTATG AGGGTCCATC TGACTCCTTC AAGGCCCTTG TGGATATGGC AGCTGTGCAT 1320

TCATCGTGCC GTCTTTGCAT TCACTTGGCC ACAGTGAGTA GAGAGAAGGA AGAAAATAAT 1380

CCAAGCCTTA AGAGACGTCC TTGCAAGTGC ACTAGAGGGC CAGAAACCGT ATATCATATC 1440

TATGTCAGAG AAAGGGGAAG GTTTGAGATG GAGTCCATTT ACCTGAGGTC TAGCAATTTA 1500

ACTCTGAATG CTGTGAAGGC TGCTGTTGTT TTGAAGTTCA CATCCCTGAA TCTTGTGCCT 1560

GTATGGAAGA CTGAAAGGCC TGAAGTTATA AGAGGGGGGA GTGCTTTAAA ACTCTACAAA 1620

ATATACCCAA TTGGCTTGAC ACAGAGACAA GCTCTTTATA CCTTCAGCTT CAAAGGTGAT 1680

GCTGATTTCA GGAGTCACTT GGAGAACAAT CCTTGTGCCA AGTTTGAAGT CATTTTTGTG 1740

TAGCATGCGC TAAATGGTAC CTCTGCTCTA CCTGAATTAG CTTCACTTAG CTGAGCACTA 1800

GCTAGAGTTT TAGGAATGAG TATGGCAGTG AATATGGCAT GGCTTTATTT ATGCCTAGTT 1860

TCTTGGCCAA CTCATTGATG TTTTGTATAA GACATCACAC TTTAATTTTA AACTTGTTTC 1920

TGTAGAAGTG CAAATCCATA TTTAATGCTT AGTTTTAGTG CTCTTATCTG ATCATCTAGA 1980

AGTCACAGTT CTTGTATATT GTGAGTGAAA ACTGAAATCT AATAGAAGGA TCAGATGTTT 2040

CACTCAAGAC ACATTATTAC TTCATGTTGT TTTGATGATC TCGAGCTTTT TTAGTGTCTG 2100

GAACTGTCCC TGTGGTTTGA GCACCTGTTA TTGCTTCAGT GTTACTGTCC AGTGGTTATC 2160

GTTTTTGACC TCTAAAAAAA AAAAAAAAAA AAAAAAAA 2198

FIG.5 b

```
Met Met Gly Leu Leu Thr Asn Leu Arg Gly Ser Arg Thr Asp Gly Ala
1               5                  10                  15

Gln Gln Asp Ser Leu Pro Val Leu Ala Pro Gly Gly Asn Pro Lys Arg
            20                  25                  30

Lys Trp Ser Asn Leu Met Pro Leu Val Val Ala Leu Val Val Ile Ala
        35                  40                  45

Glu Ile Ala Phe Leu Gly Arg Leu Asp Met Ala Lys Asn Ala Ala Met
    50                  55                  60

Val Asp Ser Leu Ala Asp Phe Phe Tyr Arg Ser Arg Ala Val Val Glu
65                  70                  75                  80

Gly Asp Asp Leu Gly Leu Gly Leu Val Ala Ser Asp Arg Asn Ser Glu
                85                  90                  95

Ser Tyr Ser Cys Glu Glu Trp Leu Glu Arg Glu Asp Ala Val Thr Tyr
            100                 105                 110

Ser Arg Gly Phe Ser Lys Glu Pro Ile Phe Val Ser Gly Ala Asp Gln
        115                 120                 125

Glu Trp Lys Ser Cys Ser Val Gly Cys Lys Phe Gly Phe Ser Gly Asp
    130                 135                 140

Arg Lys Pro Asp Ala Ala Phe Gly Leu Pro Gln Pro Ser Gly Thr Ala
145                 150                 155                 160

Ser Ile Leu Arg Ser Met Glu Ser Ala Glu Tyr Tyr Ala Glu Asn Asn
                165                 170                 175

Ile Ala Met Ala Arg Arg Arg Gly Tyr Asn Ile Val Met Thr Thr Ser
            180                 185                 190

Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp Ala Glu Tyr Asp
        195                 200                 205

Met Met Ala Pro Val Gln Pro Lys Thr Glu Ala Ala Leu Ala Ala Ala
    210                 215                 220

Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu Gln Ala Leu Glu
225                 230                 235                 240

Ala Leu Glu Lys Ser Asn Ile Lys Ile Asp Ser Tyr Gly Gly Cys His
```

FIG.6 a

```
Arg Asn Arg Asp Gly Arg Val Asn Lys Val Glu Ala Leu Lys His Tyr
            260                 265                 270

Lys Phe Ser Leu Ala Phe Glu Asn Ser Asn Glu Glu Asp Tyr Val Thr
        275                 280                 285

Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Thr Val Pro Val Val Val
    290                 295                 300

Gly Ala Pro Asn Ile Gln Asp Phe Ala Pro Ser Pro Gly Ser Ile Leu
305                 310                 315                 320

His Ile Lys Glu Ile Glu Asp Val Glu Ser Val Ala Lys Thr Met Arg
                325                 330                 335

Tyr Leu Ala Glu Asn Pro Glu Ala Tyr Asn Gln Ser Leu Arg Trp Lys
            340                 345                 350

Tyr Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val Asp Met Ala Ala
        355                 360                 365

Val His Ser Ser Cys Arg Leu Cys Ile His Leu Ala Thr Val Ser Arg
    370                 375                 380

Glu Lys Glu Glu Asn Asn Pro Ser Leu Lys Arg Arg Pro Cys Lys Cys
385                 390                 395                 400

Thr Arg Gly Pro Glu Thr Val Tyr His Ile Tyr Val Arg Glu Arg Gly
                405                 410                 415

Arg Phe Glu Met Glu Ser Ile Tyr Leu Arg Ser Ser Asn Leu Thr Leu
            420                 425                 430

Asn Ala Val Lys Ala Ala Val Val Leu Lys Phe Thr Ser Leu Asn Leu
        435                 440                 445

Val Pro Val Trp Lys Thr Glu Arg Pro Glu Val Ile Arg Gly Gly Ser
    450                 455                 460

Ala Leu Lys Leu Tyr Lys Ile Tyr Pro Ile Gly Leu Thr Gln Arg Gln
465                 470                 475                 480

Ala Leu Tyr Thr Phe Ser Phe Lys Gly Asp Ala Asp Phe Arg Ser His
                485                 490                 495

Leu Glu Asn Asn Pro Cys Ala Lys Phe Glu Val Ile Phe Val
            500                 505                 510
```

FIG.6 b

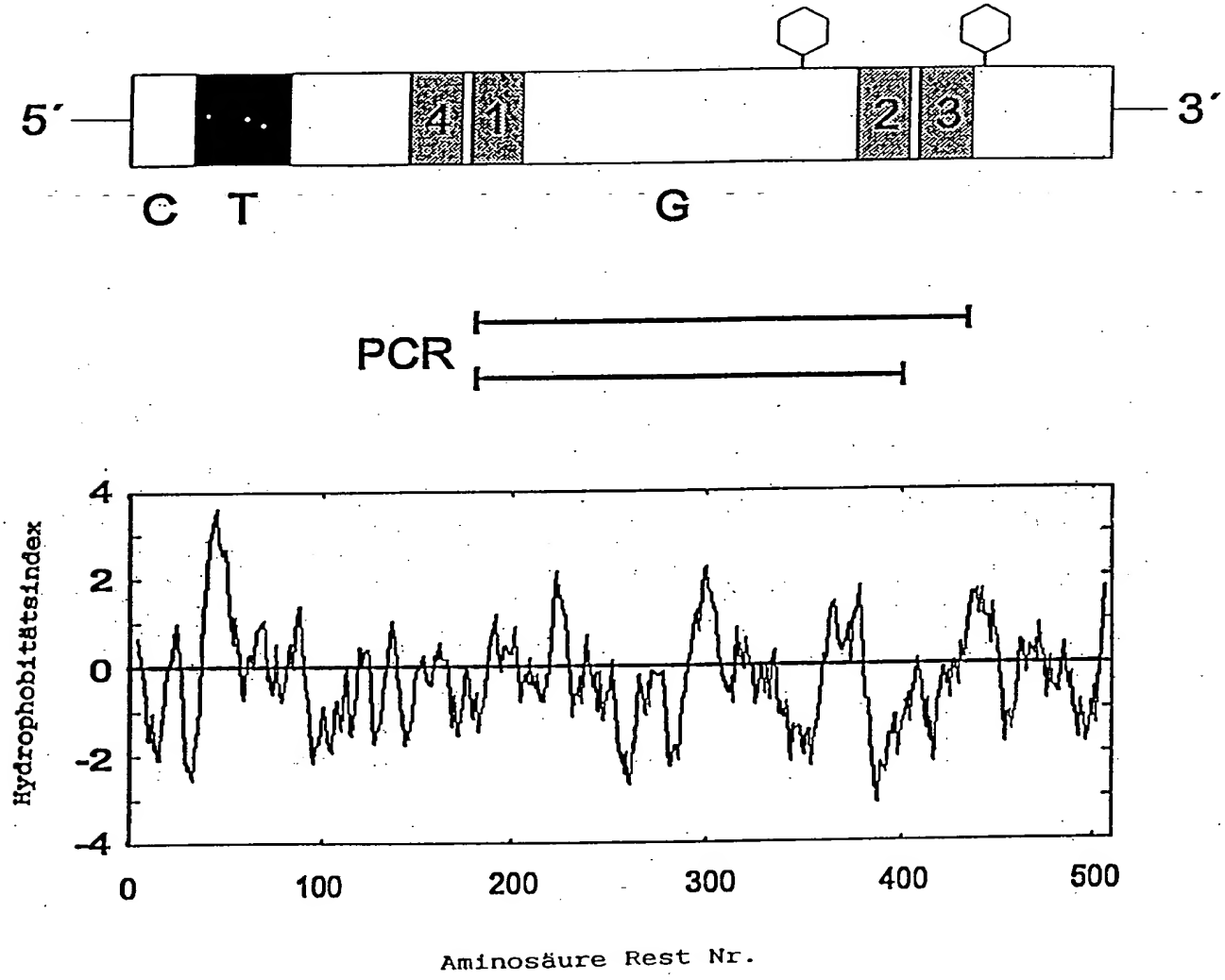

5'
4
1
2
3
3'
C
T
G
PCR
Hydrophobitätsindex
4
2
0
-2
-4
0
100
200
300
400
500
Aminosäure Rest Nr.

FIG.7

Transferase	Art	#[a]	konserviertes Motiv
FucT-C3	Mungo Bohne		267-EALKHYKFSLAFENSNEEDYVTEKFFQ-SLVAGTVP
FucT-III	Mensch	P21217	236-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-III	Schimpanse	O19058	247-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-V	Mensch	Q11128	249-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-V	Schimpanse	P56433	249-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-VI	Mensch	P51993	235-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-VI	Schimpanse	P56434	235-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
Fuc-T-III	Rind	Q11126	240-KQLSQYKFYLAFENSLHPDYITEKLWRNALQAWAVP
Fuc-T-?	chin. Hamster	O35886	237-GTLARYKFYLAFENSLHPDYITEKLWKNALEAWAVP
FucT-VII	Mensch	Q11130	217-PTVAQYRFYLSFENSQHRDYITEKFWRNALVAGTVP
FucT-VII	Maus	Q11131	264-PTLARYRFYLAFENSQHRDYITEKFWRNALAAGAVP
FucT-VII	*Schistosoma mansonii*	O76204	226-PTLARYRFYLAFENSQHRDYITEKFWRNALAAGAVP
FucT-IV	Mensch	P22083	277-HTVARYKFYLAFENSQHLDYITEKLWRNALLAGAVP
FucT-IV	Maus	Q11127	305-HTVARYKFYLAFENSRHVDYITEKLWRNAFLAGAVP
FucT-IV	Ratte	Q62994	305-HTVARYKFYLAFENSQHVDYNTEKLWRNAFLAGAVP
FucT-IV	Huhn	Q98952	228-KTVSAYKFYLAFENSQHTDYITEKLWKNAFAASAVP
FucT-IX	Maus	O88819	233-PTISTCKFYLSFENSIHKDYITEKLYNAFL-AGSVP
FutA	*Dictyostelium discoideum*	O76544	247 -DVLKRYNFAIAFENSLCKDYITEKLWE-SLSVGTIP
hpFucT1	*Helicobacter pylori*	O32631	106 -EFLSQYKFNLCFENSQGYGYVTEKILD-AYFSHTIP
hpFucT2	*Helicobacter pylori*	O30511	227 -EFLSQYKFNLCFENTQGYGYVTEKIID-AYFSHTIP
CEFT-1	*Caenorhabditis elegans*	Q21362	303-MLDTDYHFYVTFENSICEDYVTEKLWKSGYQNTIIP

[a] Zugriffsnummer für die SwissProt Protein Sequenz Datenbank

FIG.8

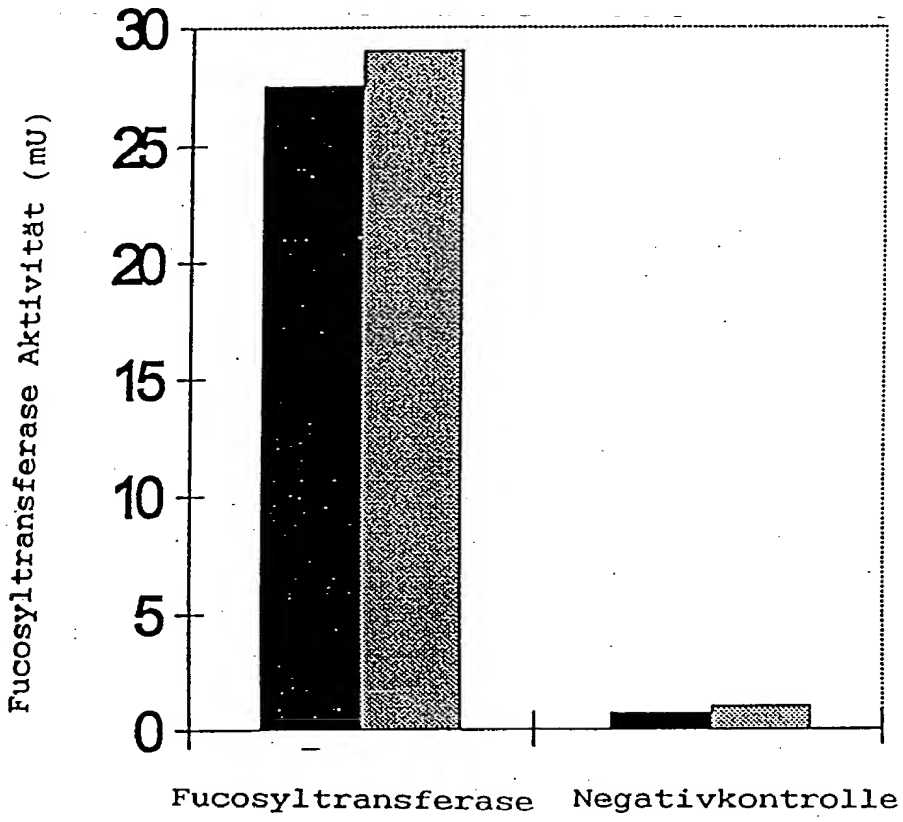
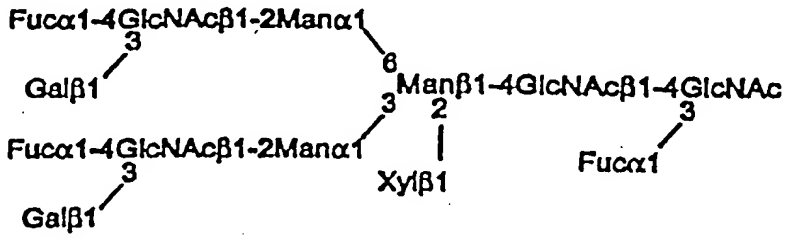
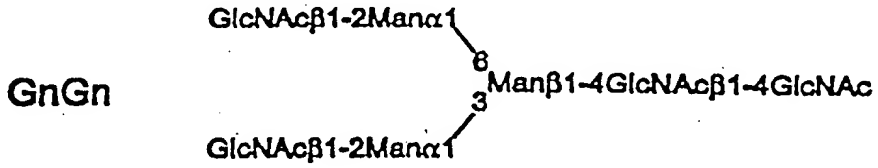
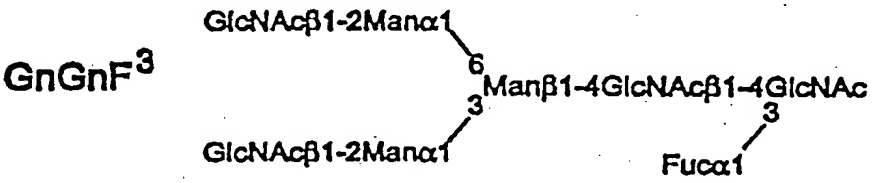
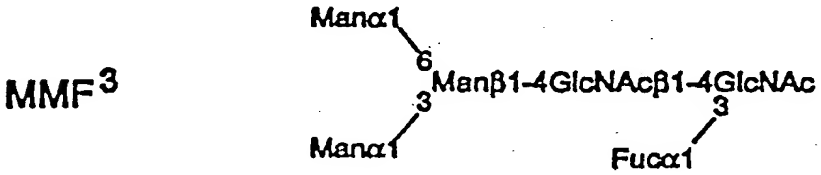

Fucosyltransferase Aktivität (mU)
30
25
20
15
10
5
0
Fucosyltransferase
Negativkontrolle

FIG.9


Fucα1-4GlcNAcβ1-2Manα1
3
Galβ1
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
2
Fucα1-4GlcNAcβ1-2Manα1
3
Galβ1
Xylβ1
3
Fucα1


GnGn
GlcNAcβ1-2Manα1
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
GlcNAcβ1-2Manα1


GnGnF3
GlcNAcβ1-2Manα1
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
3
GlcNAcβ1-2Manα1
Fucα1


MMF3
Manα1
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
3
Manα1
Fucα1

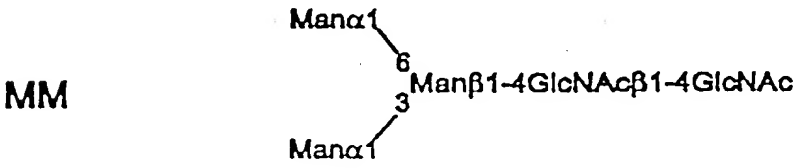

MM
Manα1
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
Manα1

FIG.10 a

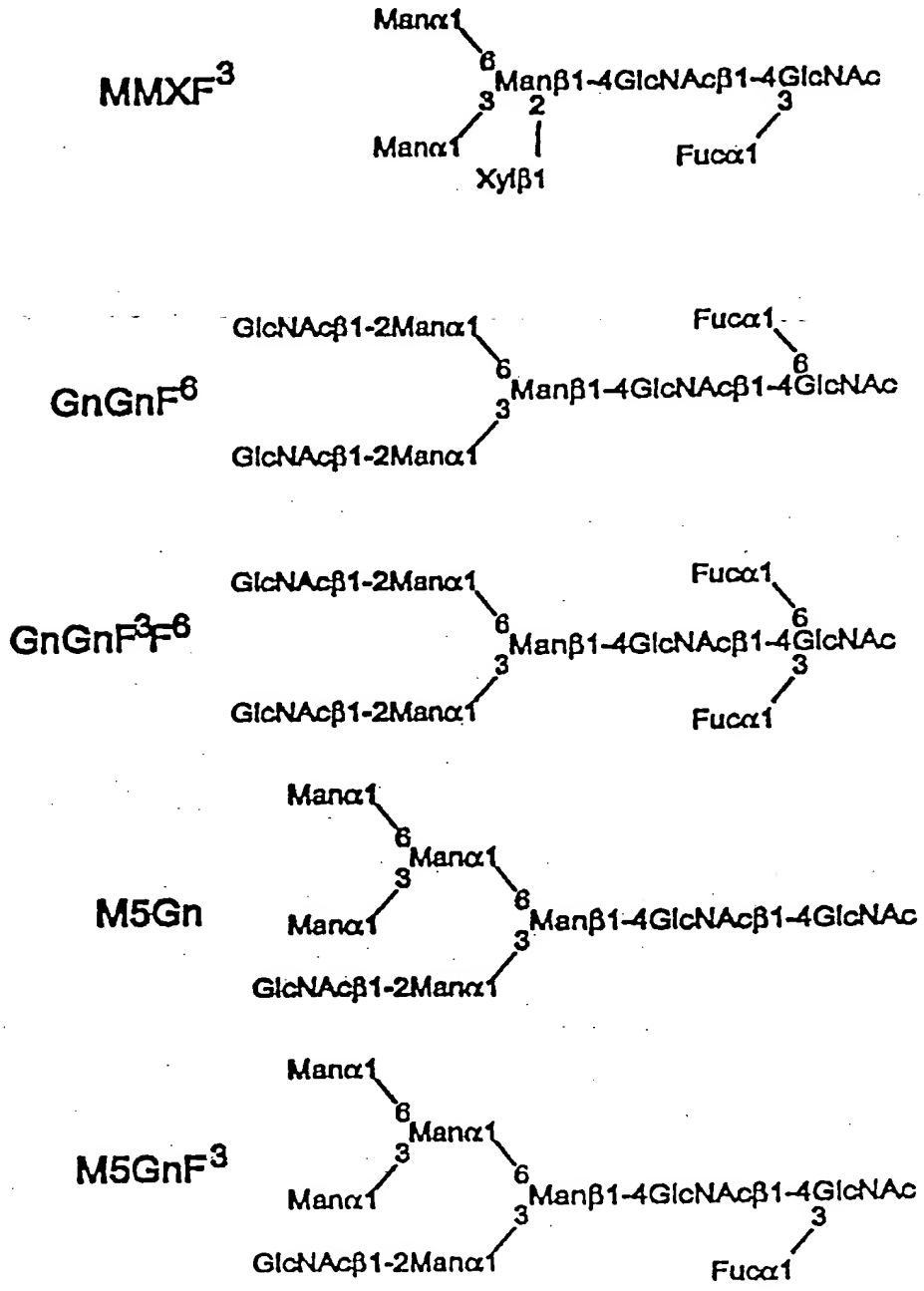

MMXF3
Manα1
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
2
3
Manα1
Xylβ1
Fucα1
GnGnF6
GlcNAcβ1-2Manα1
Fucα1
6
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
GlcNAcβ1-2Manα1
GnGnF3F6
GlcNAcβ1-2Manα1
Fucα1
6
6
Manβ1-4GlcNAcβ1-4GlcNAc
3
3
GlcNAcβ1-2Manα1
Fucα1
M5Gn
Manα1
6
Manα1
3
6
Manβ1-4GlcNAcβ1-4GlcNAc
Manα1
3
GlcNAcβ1-2Manα1
M5GnF3
Manα1
6
Manα1
3
6
Manβ1-4GlcNAcβ1-4GlcNAc
Manα1
3
3
GlcNAcβ1-2Manα1
Fucα1

FIG.10 b

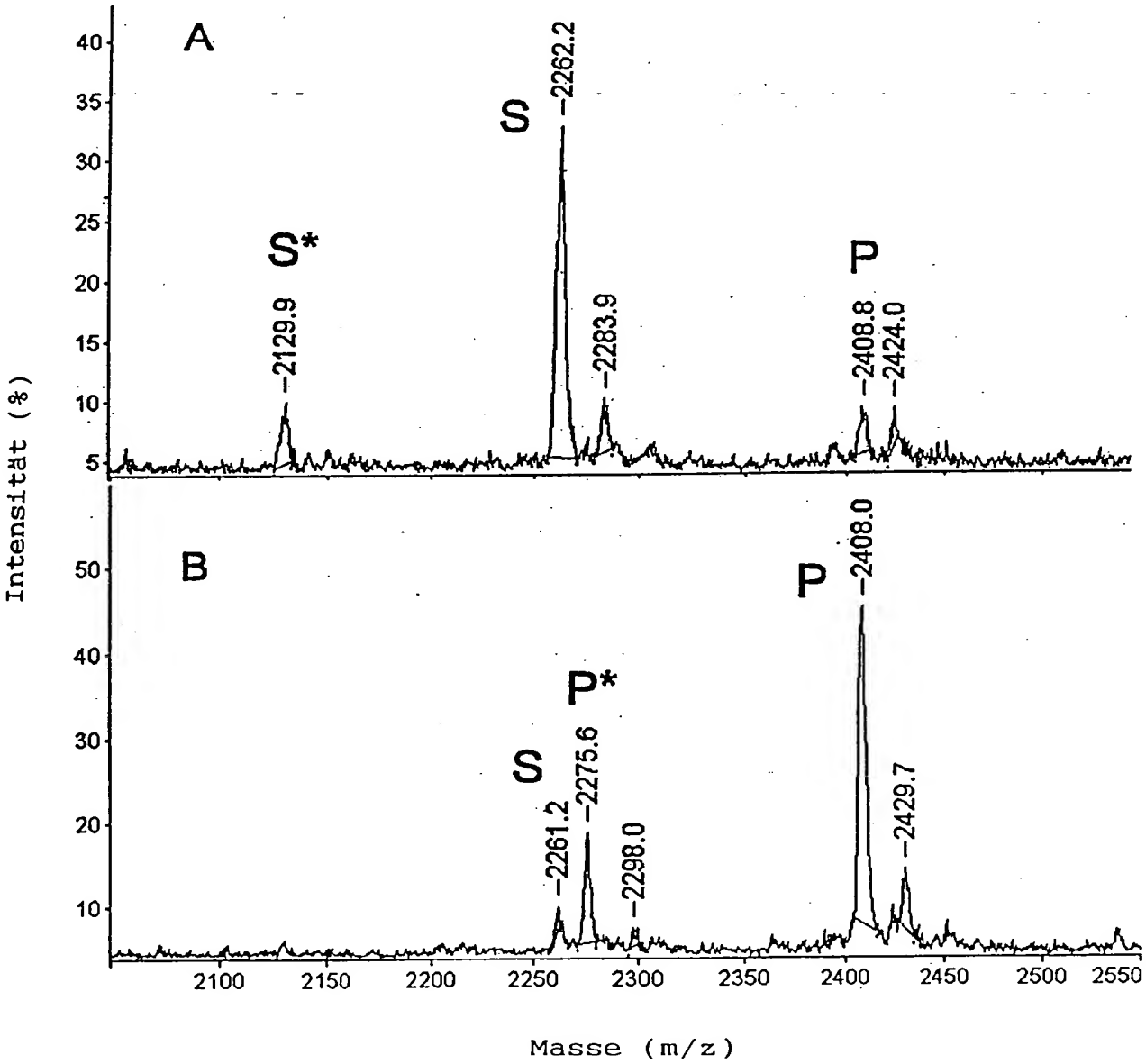
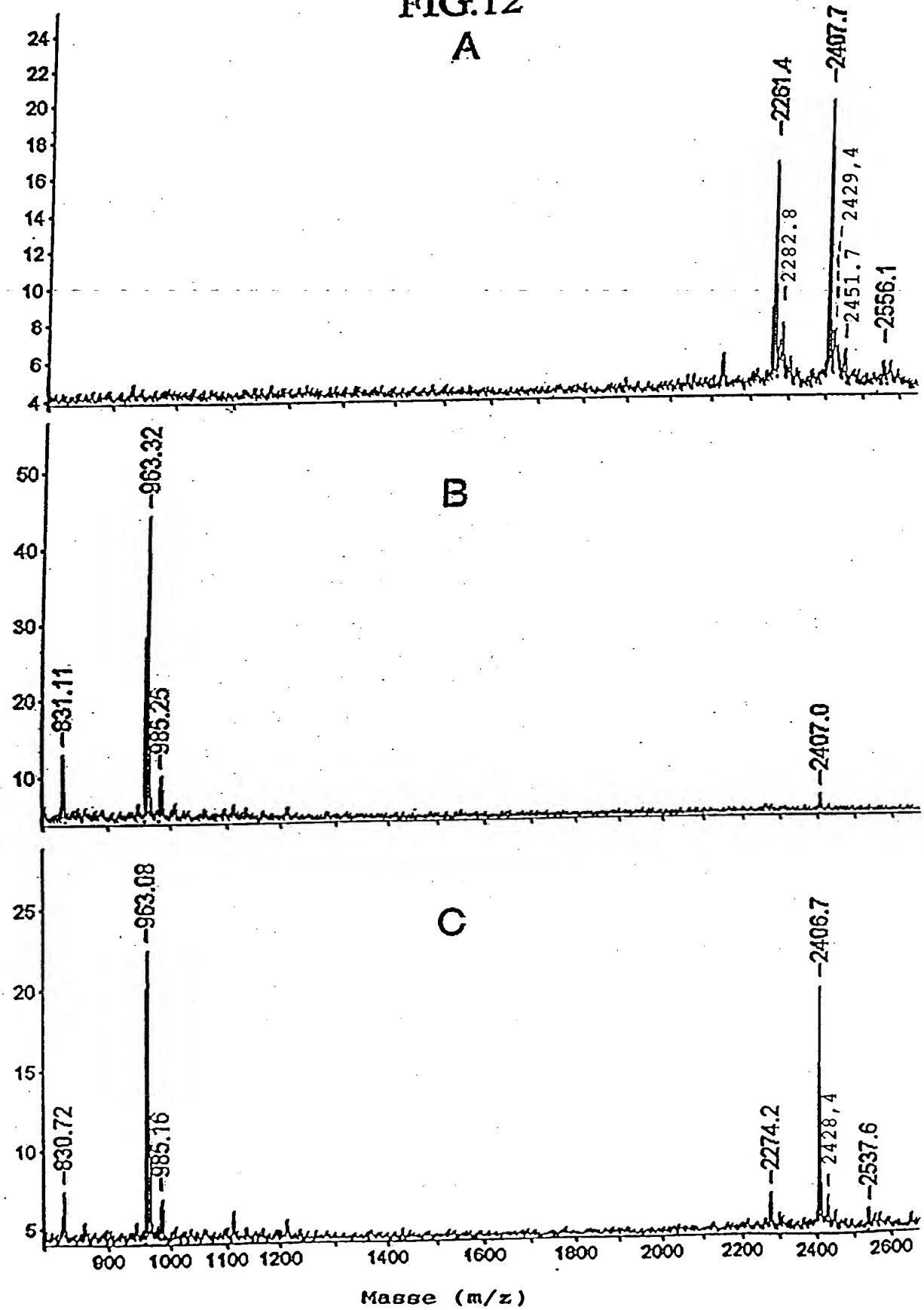

A
S*
-2129.9
S
-2262.2
-2283.9
P
-2408.8
-2424.0
B
P
-2408.0
P*
S
-2261.2
-2275.6
-2298.0
-2429.7
Intensität (%)
Masse (m/z)
40
35
30
25
20
15
10
5
50
40
30
20
10
2100
2150
2200
2250
2300
2350
2400
2450
2500
2550

FIG.11

FIG.12


A
-2261.4
-2407.7
-2282.8
-2429,4
-2451.7
-2556.1
B
-963.32
-831.11
-985.25
-2407.0
C
-963.08
-2406.7
-830.72
-985.16
-2274.2
-2428,4
-2537.6
Masse (m/z)

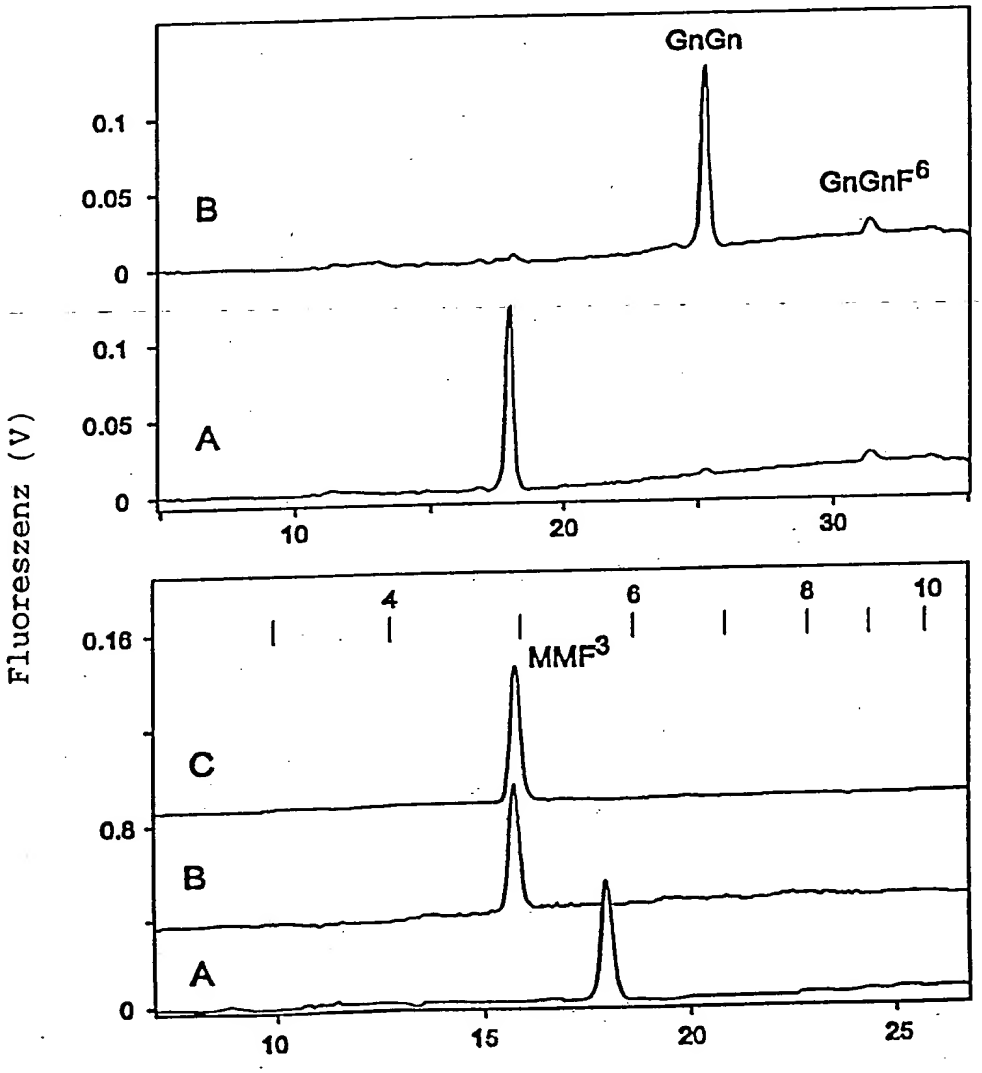

GnGn
GnGnF6
B
A
0.1
0.05
0
10
20
30
4
6
8
10
MMF3
C
B
A
0.16
0.8
0
10
15
20
25
Fluoreszenz (V)
Elutionszeit (min)

FIG.13